SEQUENCE LISTING

<110> White, David
     Tayber, Olga

<120> 84569, A NOVEL HUMAN MAP KINASE FAMILY
   MEMBER AND USES THEREFOR

<130> MPI02-128P1RM

<150> 60/395,943
<151> 2002-07-15

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<170> FastSEQ for Windows Version 4.0

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aaa aag caa tca ttt cct tgc atc tgt aaa aat cca gga aca cag aag     96
Lys Lys Gln Ser Phe Pro Cys Ile Cys Lys Asn Pro Gly Thr Gln Lys
             20                  25                  30

tca tgt gtt cct ctc tct gtt caa ccg aca gag cca aga cta aat tac    144
Ser Cys Val Pro Leu Ser Val Gln Pro Thr Glu Pro Arg Leu Asn Tyr
         35                  40                  45

cta gat ctt aag tat agt gat atg ttc aaa gaa atc aat tca act gct    192
Leu Asp Leu Lys Tyr Ser Asp Met Phe Lys Glu Ile Asn Ser Thr Ala
     50                  55                  60

aat gga cct gga atc tat gaa atg ttt ggg acc cct gtt tat tgt cat    240
Asn Gly Pro Gly Ile Tyr Glu Met Phe Gly Thr Pro Val Tyr Cys His
 65                  70                  75                  80

gtg cga gag act gaa agg gat gaa aac acg tat tac cgt gag ata tgt    288
Val Arg Glu Thr Glu Arg Asp Glu Asn Thr Tyr Tyr Arg Glu Ile Cys
                 85                  90                  95

tcg gct cca tca ggc aga cgt atc acc aat aaa tgt cga tct tca cac    336
Ser Ala Pro Ser Gly Arg Arg Ile Thr Asn Lys Cys Arg Ser Ser His
            100                 105                 110

agt gag agg aag agc aat atc aga aca aga ctt tct cag aaa aaa aca    384
Ser Glu Arg Lys Ser Asn Ile Arg Thr Arg Leu Ser Gln Lys Lys Thr
        115                 120                 125

cat atg aaa tgc cca aag act tca ttt ggc att aaa caa gag cac aaa    432
His Met Lys Cys Pro Lys Thr Ser Phe Gly Ile Lys Gln Glu His Lys
        130                 135                 140

gtc tta att tct aaa gaa aag agt tcc aag gct gta cat agc aac cta    480
Val Leu Ile Ser Lys Glu Lys Ser Ser Lys Ala Val His Ser Asn Leu
145                 150                 155                 160
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1

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cat gac att gaa aat ggt gat ggt att tca gaa cca gac tgg cag ata      528
His Asp Ile Glu Asn Gly Asp Gly Ile Ser Glu Pro Asp Trp Gln Ile
                165                 170                 175

aag tct tca gga aat gag ttt cta tct tcc aaa gat gaa att cat ccc      576
Lys Ser Ser Gly Asn Glu Phe Leu Ser Ser Lys Asp Glu Ile His Pro
                180                 185                 190

atg aac ttg gct cag aca cct gag cag tcc atg aaa cag aat gaa ttc      624
Met Asn Leu Ala Gln Thr Pro Glu Gln Ser Met Lys Gln Asn Glu Phe
            195                 200                 205

cct cct gtc tca gat tta tcc att gtt gaa gaa gtt tct atg gaa gag      672
Pro Pro Val Ser Asp Leu Ser Ile Val Glu Glu Val Ser Met Glu Glu
    210                 215                 220

tct act ggt gat aga gac att tct aac aat caa ata ctc acc aca agc      720
Ser Thr Gly Asp Arg Asp Ile Ser Asn Asn Gln Ile Leu Thr Thr Ser
225                 230                 235                 240

ctc aga gat ctg caa gaa ctt gaa gag cta cat cac cag atc cca ttt      768
Leu Arg Asp Leu Gln Glu Leu Glu Glu Leu His His Gln Ile Pro Phe
                245                 250                 255

atc cct tca gaa gac agc tgg gca gtg ccc agt gag aag aat tct aac      816
Ile Pro Ser Glu Asp Ser Trp Ala Val Pro Ser Glu Lys Asn Ser Asn
                260                 265                 270

aag tat gta cag caa gaa aag cag aat aca gca tct ctt agt aaa gta      864
Lys Tyr Val Gln Gln Glu Lys Gln Asn Thr Ala Ser Leu Ser Lys Val
            275                 280                 285

aat gcc agc cga att tta act aat gat cta gag ttt gat agt gtt tca      912
Asn Ala Ser Arg Ile Leu Thr Asn Asp Leu Glu Phe Asp Ser Val Ser
    290                 295                 300

gat cac tct aaa aca ctt aca aat ttc tct ttc caa gca aaa caa gaa      960
Asp His Ser Lys Thr Leu Thr Asn Phe Ser Phe Gln Ala Lys Gln Glu
305                 310                 315                 320

agt gca tct tcc cag aca tat caa tat tgg gta cat tat ttg gat cat     1008
Ser Ala Ser Ser Gln Thr Tyr Gln Tyr Trp Val His Tyr Leu Asp His
                325                 330                 335

gat agt tta gca aat aag tca atc aca tat caa atg ttt gga aaa acc     1056
Asp Ser Leu Ala Asn Lys Ser Ile Thr Tyr Gln Met Phe Gly Lys Thr
            340                 345                 350

tta agt ggc aca aat tca att tcc caa gaa att atg gac tct gta aat     1104
Leu Ser Gly Thr Asn Ser Ile Ser Gln Glu Ile Met Asp Ser Val Asn
            355                 360                 365

aat gaa gaa ttg aca gat gaa cta tta ggt tgt cta gct gca gaa tta     1152
Asn Glu Glu Leu Thr Asp Glu Leu Leu Gly Cys Leu Ala Ala Glu Leu
    370                 375                 380

ttg gct ctt gat gag aaa gat aac aac tct tgc caa aaa atg gca aat     1200
Leu Ala Leu Asp Glu Lys Asp Asn Asn Ser Cys Gln Lys Met Ala Asn
385                 390                 395                 400

gaa aca gat cct gaa aac cta aat ctt gtc ctc aga tgg aga gga agt     1248
Glu Thr Asp Pro Glu Asn Leu Asn Leu Val Leu Arg Trp Arg Gly Ser
                405                 410                 415

acc cca aaa gaa atg ggc aga gag aca aca aaa gtc aaa ata cag agg     1296
Thr Pro Lys Glu Met Gly Arg Glu Thr Thr Lys Val Lys Ile Gln Arg
            420                 425                 430

cat agt agt ggg ctc agg ata tat gac agg gag gag aaa ttt ctc atc     1344
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2

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His Ser Ser Gly Leu Arg Ile Tyr Asp Arg Glu Glu Lys Phe Leu Ile
        435                 440                 445

tca aat gaa aag aag ata ttt tct gaa aat agt tta aag tct gaa gaa    1392
Ser Asn Glu Lys Lys Ile Phe Ser Glu Asn Ser Leu Lys Ser Glu Glu
        450                 455                 460

cct atc cta tgg acc aag ggt gag att ctt gga aag gga gcc tac ggc    1440
Pro Ile Leu Trp Thr Lys Gly Glu Ile Leu Gly Lys Gly Ala Tyr Gly
465                 470                 475                 480

aca gta tac tgt ggt ctc act agt caa gga cag cta ata gct gta aaa    1488
Thr Val Tyr Cys Gly Leu Thr Ser Gln Gly Gln Leu Ile Ala Val Lys
                485                 490                 495

cag gtg gct ttg gat acc tct aat aaa tta gct gct gaa aag gaa tac    1536
Gln Val Ala Leu Asp Thr Ser Asn Lys Leu Ala Ala Glu Lys Glu Tyr
                500                 505                 510

cgg aaa cta cag gaa gaa gta gat ttg ctc aaa gca ctg aaa cat gtc    1584
Arg Lys Leu Gln Glu Glu Val Asp Leu Leu Lys Ala Leu Lys His Val
                515                 520                 525

aac att gtg gcc tat ttg ggg aca tgc ttg caa gag aac act gtg agc    1632
Asn Ile Val Ala Tyr Leu Gly Thr Cys Leu Gln Glu Asn Thr Val Ser
        530                 535                 540

att ttc atg gag ttt gtt cct ggt ggc tca atc tct agt att ata aac    1680
Ile Phe Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser Ile Ile Asn
545                 550                 555                 560

cgt ttt ggg cca ttg cct gag atg gtg ttc tgt aaa tat acg aaa caa    1728
Arg Phe Gly Pro Leu Pro Glu Met Val Phe Cys Lys Tyr Thr Lys Gln
                565                 570                 575

ata ctt caa ggt gtt gct tat ctc cat gag aac tgt gtg gta cat cgc    1776
Ile Leu Gln Gly Val Ala Tyr Leu His Glu Asn Cys Val Val His Arg
                580                 585                 590

gat atc aaa gga aat aat gtt atg ctc atg cca act gga ata ata aag    1824
Asp Ile Lys Gly Asn Asn Val Met Leu Met Pro Thr Gly Ile Ile Lys
                595                 600                 605

ctg att gac ttt ggc tgt gcc agg cgt ttg gcc tgg gca ggt tta aat    1872
Leu Ile Asp Phe Gly Cys Ala Arg Arg Leu Ala Trp Ala Gly Leu Asn
        610                 615                 620

ggc acc cac agt gac atg ctt aag tcc atg cat ggg act cca tat tgg    1920
Gly Thr His Ser Asp Met Leu Lys Ser Met His Gly Thr Pro Tyr Trp
625                 630                 635                 640

atg gcc cca gaa gtc atc aat gag tct ggc tat gga cgg aaa tca gat    1968
Met Ala Pro Glu Val Ile Asn Glu Ser Gly Tyr Gly Arg Lys Ser Asp
                645                 650                 655

atc tgg agc att ggt tgt act gtg ttt gag atg gct aca ggg aag cct    2016
Ile Trp Ser Ile Gly Cys Thr Val Phe Glu Met Ala Thr Gly Lys Pro
                660                 665                 670

cca ctg gct tcc atg gac agg atg gcc gcc atg ttt tac atc gga gca    2064
Pro Leu Ala Ser Met Asp Arg Met Ala Ala Met Phe Tyr Ile Gly Ala
                675                 680                 685

cac cga ggg ctg atg cct cct tta cca gac cac ttc tca gaa aat gca    2112
His Arg Gly Leu Met Pro Pro Leu Pro Asp His Phe Ser Glu Asn Ala
        690                 695                 700

gca gac ttt gtg cgc atg tgc ctg acc agg gac cag cat gag cga cct    2160
Ala Asp Phe Val Arg Met Cys Leu Thr Arg Asp Gln His Glu Arg Pro


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```
tct gct ctc cag ctc ctg aag cac tcc ttc ttg gag aga agt cac tga     2208
Ser Ala Leu Gln Leu Leu Lys His Ser Phe Leu Glu Arg Ser His *
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            20                  25                  30
Ser Cys Val Pro Leu Ser Val Gln Pro Thr Glu Pro Arg Leu Asn Tyr
        35                  40                  45
Leu Asp Leu Lys Tyr Ser Asp Met Phe Lys Glu Ile Asn Ser Thr Ala
    50                  55                  60
Asn Gly Pro Gly Ile Tyr Glu Met Phe Gly Thr Pro Val Tyr Cys His
65                  70                  75                  80
Val Arg Glu Thr Glu Arg Asp Glu Asn Thr Tyr Tyr Arg Glu Ile Cys
                85                  90                  95
Ser Ala Pro Ser Gly Arg Arg Ile Thr Asn Lys Cys Arg Ser Ser His
            100                 105                 110
Ser Glu Arg Lys Ser Asn Ile Arg Thr Arg Leu Ser Gln Lys Lys Thr
        115                 120                 125
His Met Lys Cys Pro Lys Thr Ser Phe Gly Ile Lys Gln Glu His Lys
    130                 135                 140
Val Leu Ile Ser Lys Glu Lys Ser Ser Lys Ala Val His Ser Asn Leu
145                 150                 155                 160
His Asp Ile Glu Asn Gly Asp Gly Ile Ser Glu Pro Asp Trp Gln Ile
                165                 170                 175
Lys Ser Ser Gly Asn Glu Phe Leu Ser Ser Lys Asp Glu Ile His Pro
            180                 185                 190
Met Asn Leu Ala Gln Thr Pro Glu Gln Ser Met Lys Gln Asn Glu Phe
        195                 200                 205
Pro Pro Val Ser Asp Leu Ser Ile Val Glu Glu Val Ser Met Glu Glu
    210                 215                 220
Ser Thr Gly Asp Arg Asp Ile Ser Asn Asn Gln Ile Leu Thr Thr Ser
225                 230                 235                 240
Leu Arg Asp Leu Gln Glu Leu Glu Glu Leu His His Gln Ile Pro Phe
                245                 250                 255
Ile Pro Ser Glu Asp Ser Trp Ala Val Pro Ser Glu Lys Asn Ser Asn
            260                 265                 270
Lys Tyr Val Gln Gln Glu Lys Gln Asn Thr Ala Ser Leu Ser Lys Val
        275                 280                 285
Asn Ala Ser Arg Ile Leu Thr Asn Asp Leu Glu Phe Asp Ser Val Ser
    290                 295                 300
Asp His Ser Lys Thr Leu Thr Asn Phe Ser Phe Gln Ala Lys Gln Glu
305                 310                 315                 320
Ser Ala Ser Ser Gln Thr Tyr Gln Tyr Trp Val His Tyr Leu Asp His
                325                 330                 335
Asp Ser Leu Ala Asn Lys Ser Ile Thr Tyr Gln Met Phe Gly Lys Thr
            340                 345                 350
Leu Ser Gly Thr Asn Ser Ile Ser Gln Glu Ile Met Asp Ser Val Asn
        355                 360                 365
Asn Glu Glu Leu Thr Asp Glu Leu Leu Gly Cys Leu Ala Ala Glu Leu
    370                 375                 380
Leu Ala Leu Asp Glu Lys Asp Asn Asn Ser Cys Gln Lys Met Ala Asn
385                 390                 395                 400
Glu Thr Asp Pro Glu Asn Leu Asn Leu Val Leu Arg Trp Arg Gly Ser
                405                 410                 415
Thr Pro Lys Glu Met Gly Arg Glu Thr Thr Lys Val Lys Ile Gln Arg
            420                 425                 430
His Ser Ser Gly Leu Arg Ile Tyr Asp Arg Glu Glu Lys Phe Leu Ile
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4

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              435                        440                        445
Ser Asn Glu Lys Lys Ile Phe Ser Glu Asn Ser Leu Lys Ser Glu Glu
    450                        455                        460
Pro Ile Leu Trp Thr Lys Gly Glu Ile Leu Gly Lys Gly Ala Tyr Gly
465                        470                        475                 480
Thr Val Tyr Cys Gly Leu Thr Ser Gln Gly Gln Leu Ile Ala Val Lys
              485                        490                        495
Gln Val Ala Leu Asp Thr Ser Asn Lys Leu Ala Ala Glu Lys Glu Tyr
              500                        505                        510
Arg Lys Leu Gln Glu Glu Val Asp Leu Leu Lys Ala Leu Lys His Val
              515                        520                        525
Asn Ile Val Ala Tyr Leu Gly Thr Cys Leu Gln Glu Asn Thr Val Ser
              530                        535                        540
Ile Phe Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser Ile Ile Asn
545                        550                        555                 560
Arg Phe Gly Pro Leu Pro Glu Met Val Phe Cys Lys Tyr Thr Lys Gln
              565                        570                        575
Ile Leu Gln Gly Val Ala Tyr Leu His Glu Asn Cys Val Val His Arg
              580                        585                        590
Asp Ile Lys Gly Asn Asn Val Met Leu Met Pro Thr Gly Ile Ile Lys
              595                        600                        605
Leu Ile Asp Phe Gly Cys Ala Arg Arg Leu Ala Trp Ala Gly Leu Asn
              610                        615                        620
Gly Thr His Ser Asp Met Leu Lys Ser Met His Gly Thr Pro Tyr Trp
625                        630                        635                 640
Met Ala Pro Glu Val Ile Asn Glu Ser Gly Tyr Gly Arg Lys Ser Asp
              645                        650                        655
Ile Trp Ser Ile Gly Cys Thr Val Phe Glu Met Ala Thr Gly Lys Pro
              660                        665                        670
Pro Leu Ala Ser Met Asp Arg Met Ala Ala Met Phe Tyr Ile Gly Ala
              675                        680                        685
His Arg Gly Leu Met Pro Pro Leu Pro Asp His Phe Ser Glu Asn Ala
              690                        695                        700
Ala Asp Phe Val Arg Met Cys Leu Thr Arg Asp Gln His Glu Arg Pro
705                        710                        715                 720
Ser Ala Leu Gln Leu Leu Lys His Ser Phe Leu Glu Arg Ser His
              725                        730                        735
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<213> Homo sapiens

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Met Pro Gln Ile Ala Lys Lys Gln Ser Thr His Arg Thr Gln Lys Pro
 1               5                  10                  15

aaa aag caa tca ttt cct tgc atc tgt aaa aat cca gga aca cag aag   96
Lys Lys Gln Ser Phe Pro Cys Ile Cys Lys Asn Pro Gly Thr Gln Lys
                 20                  25                  30

tca tgt gtt cct ctc tct gtt caa ccg aca gag cca aga cta aat tac  144
Ser Cys Val Pro Leu Ser Val Gln Pro Thr Glu Pro Arg Leu Asn Tyr
                 35                  40                  45

cta gat ctt aag tat agt gat atg ttc aaa gaa atc aat tca act gct  192
Leu Asp Leu Lys Tyr Ser Asp Met Phe Lys Glu Ile Asn Ser Thr Ala
         50                  55                  60

aat gga cct gga atc tat gaa atg ttt ggg acc cct gtt tat tgt cat  240
Asn Gly Pro Gly Ile Tyr Glu Met Phe Gly Thr Pro Val Tyr Cys His
 65                  70                  75                  80
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gtg cga gag act gaa agg gat gaa aac acg tat tac cgt gag ata tgt    288
Val Arg Glu Thr Glu Arg Asp Glu Asn Thr Tyr Tyr Arg Glu Ile Cys
                    85                  90                  95

tcg gct cca tca ggc aga cgt atc acc aat aaa tgt cga tct tca cac    336
Ser Ala Pro Ser Gly Arg Arg Ile Thr Asn Lys Cys Arg Ser Ser His
            100                 105                 110

agt gag agg aag agc aat atc aga aca aga ctt tct cag aaa aaa aca    384
Ser Glu Arg Lys Ser Asn Ile Arg Thr Arg Leu Ser Gln Lys Lys Thr
            115                 120                 125

cat atg aaa tgc cca aag act tca ttt ggc att aaa caa gag cac aaa    432
His Met Lys Cys Pro Lys Thr Ser Phe Gly Ile Lys Gln Glu His Lys
    130                 135                 140

gtc tta att tct aaa gaa aag agt tcc aag gct gta cat agc aac cta    480
Val Leu Ile Ser Lys Glu Lys Ser Ser Lys Ala Val His Ser Asn Leu
145             150                 155                 160

cat gac att gaa aat ggt gat ggt att tca gaa cca gac tgg cag ata    528
His Asp Ile Glu Asn Gly Asp Gly Ile Ser Glu Pro Asp Trp Gln Ile
                165                 170                 175

aag tct tca gga aat gag ttt cta tct tcc aaa gat gaa att cat ccc    576
Lys Ser Ser Gly Asn Glu Phe Leu Ser Ser Lys Asp Glu Ile His Pro
            180                 185                 190

atg aac ttg gct cag aca cct gag cag tcc atg aaa cag aat gaa ttc    624
Met Asn Leu Ala Gln Thr Pro Glu Gln Ser Met Lys Gln Asn Glu Phe
            195                 200                 205

cct cct gtc tca gat tta tcc att gtt gaa gaa gtt tct atg gaa gag    672
Pro Pro Val Ser Asp Leu Ser Ile Val Glu Glu Val Ser Met Glu Glu
    210                 215                 220

tct act ggt gat aga gac att tct aac aat caa ata ctc acc aca agc    720
Ser Thr Gly Asp Arg Asp Ile Ser Asn Asn Gln Ile Leu Thr Thr Ser
225                 230                 235                 240

ctc aga gat ctg caa gaa ctt gaa gag cta cat cac cag atc cca ttt    768
Leu Arg Asp Leu Gln Glu Leu Glu Glu Leu His His Gln Ile Pro Phe
                245                 250                 255

atc cct tca gaa gac agc tgg gca gtg ccc agt gag aag aat tct aac    816
Ile Pro Ser Glu Asp Ser Trp Ala Val Pro Ser Glu Lys Asn Ser Asn
                260                 265                 270

aag tat gta cag caa gaa aag cag aat aca gca tct ctt agt aaa gta    864
Lys Tyr Val Gln Gln Glu Lys Gln Asn Thr Ala Ser Leu Ser Lys Val
            275                 280                 285

aat gcc agc cga att tta act aat gat cta gag ttt gat agt gtt tca    912
Asn Ala Ser Arg Ile Leu Thr Asn Asp Leu Glu Phe Asp Ser Val Ser
    290                 295                 300

gat cac tct aaa aca ctt aca aat ttc tct ttc caa gca aaa caa gaa    960
Asp His Ser Lys Thr Leu Thr Asn Phe Ser Phe Gln Ala Lys Gln Glu
305                 310                 315                 320

agt gca tct tcc cag aca tat caa tat tgg gta cat tat ttg gat cat    1008
Ser Ala Ser Ser Gln Thr Tyr Gln Tyr Trp Val His Tyr Leu Asp His
            325                 330                 335

gat agt tta gca aat aag tca atc aca tat caa atg ttt gga aaa acc    1056
Asp Ser Leu Ala Asn Lys Ser Ile Thr Tyr Gln Met Phe Gly Lys Thr
            340                 345                 350

tta agt ggc aca aat tca att tcc caa gaa att atg gac tct gta aat    1104
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6

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            Leu Ser Gly Thr Asn Ser Ile Ser Gln Glu Ile Met Asp Ser Val Asn
                    355                 360                 365

aat gaa gaa ttg aca gat gaa cta tta ggt tgt cta gct gca gaa tta    1152
Asn Glu Glu Leu Thr Asp Glu Leu Leu Gly Cys Leu Ala Ala Glu Leu
        370                 375                 380

ttg gct ctt gat gag aaa gat aac aac tct tgc caa aaa atg gca aat    1200
Leu Ala Leu Asp Glu Lys Asp Asn Asn Ser Cys Gln Lys Met Ala Asn
385                 390                 395                 400

gaa aca gat cct gaa aac cta aat ctt gtc ctc aga tgg aga gga agt    1248
Glu Thr Asp Pro Glu Asn Leu Asn Leu Val Leu Arg Trp Arg Gly Ser
                405                 410                 415

acc cca aaa gaa atg ggc aga gag aca aca aaa gtc aaa ata cag agg    1296
Thr Pro Lys Glu Met Gly Arg Glu Thr Thr Lys Val Lys Ile Gln Arg
                420                 425                 430

cat agt agt ggg ctc agg ata tat gac agg gag gag aaa ttt ctc atc    1344
His Ser Ser Gly Leu Arg Ile Tyr Asp Arg Glu Glu Lys Phe Leu Ile
                435                 440                 445

tca aat gaa aag aag ata ttt tct gaa aat agt tta aag tct gaa gaa    1392
Ser Asn Glu Lys Lys Ile Phe Ser Glu Asn Ser Leu Lys Ser Glu Glu
        450                 455                 460

cct atc cta tgg acc aag ggt gag att ctt gga aag gga gcc tac ggc    1440
Pro Ile Leu Trp Thr Lys Gly Glu Ile Leu Gly Lys Gly Ala Tyr Gly
465                 470                 475                 480

aca gta tac tgt ggt ctc act agt caa gga cag cta ata gct gta aaa    1488
Thr Val Tyr Cys Gly Leu Thr Ser Gln Gly Gln Leu Ile Ala Val Lys
                485                 490                 495

cag gtg gct ttg gat acc tct aat aaa tta gct gct gaa aag gaa tac    1536
Gln Val Ala Leu Asp Thr Ser Asn Lys Leu Ala Ala Glu Lys Glu Tyr
                500                 505                 510

cgg aaa cta cag gaa gaa gta gat ttg ctc aaa gca ctg aaa cat gtc    1584
Arg Lys Leu Gln Glu Glu Val Asp Leu Leu Lys Ala Leu Lys His Val
                515                 520                 525

aac att gtg gcc tat ttg ggg aca tgc ttg caa gag aac act gtg agc    1632
Asn Ile Val Ala Tyr Leu Gly Thr Cys Leu Gln Glu Asn Thr Val Ser
        530                 535                 540

att ttc atg gag ttt gtt cct ggt ggc tca atc tct agt att ata aac    1680
Ile Phe Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser Ile Ile Asn
545                 550                 555                 560

cgt ttt ggg cca ttg cct gag atg gtg ttc tgt aaa tat acg aaa caa    1728
Arg Phe Gly Pro Leu Pro Glu Met Val Phe Cys Lys Tyr Thr Lys Gln
                565                 570                 575

ata ctt caa ggt gtt gct tat ctc cat gag aac tgt gtg gta cat cgc    1776
Ile Leu Gln Gly Val Ala Tyr Leu His Glu Asn Cys Val Val His Arg
                580                 585                 590

gat atc aaa gga aat aat gtt atg ctc atg cca act gga ata ata aag    1824
Asp Ile Lys Gly Asn Asn Val Met Leu Met Pro Thr Gly Ile Ile Lys
                595                 600                 605

ctg att gac ttt ggc tgt gcc agg cgt ttg gcc tgg gca ggt tta aat    1872
Leu Ile Asp Phe Gly Cys Ala Arg Arg Leu Ala Trp Ala Gly Leu Asn
                610                 615                 620

ggc acc cac agt gac atg ctt aag tcc atg cat ggg act cca tat tgg    1920
Gly Thr His Ser Asp Met Leu Lys Ser Met His Gly Thr Pro Tyr Trp
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7

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atg gcc cca gaa gtc atc aat gag tct ggc tat gga cgg aaa tca gat   1968
Met Ala Pro Glu Val Ile Asn Glu Ser Gly Tyr Gly Arg Lys Ser Asp
            645                 650                 655

atc tgg agc att ggt tgt act gtg ttt gag atg gct aca ggg aag cct   2016
Ile Trp Ser Ile Gly Cys Thr Val Phe Glu Met Ala Thr Gly Lys Pro
            660                 665                 670

cca ctg gct tcc atg gac agg atg gcc gcc atg ttt tac atc gga gca   2064
Pro Leu Ala Ser Met Asp Arg Met Ala Ala Met Phe Tyr Ile Gly Ala
            675                 680                 685

cac cga ggg ctg atg cct cct tta cca gac cac ttc tca gaa aat gca   2112
His Arg Gly Leu Met Pro Pro Leu Pro Asp His Phe Ser Glu Asn Ala
        690                 695                 700

gca gac ttt gtg cgc atg tgc ctg acc agg gac cag cat gag cga cct   2160
Ala Asp Phe Val Arg Met Cys Leu Thr Arg Asp Gln His Glu Arg Pro
705                 710                 715                 720

tct gct ctc cag ctc ctg aag cac tcc ttc ttg gag aga agt cac tga   2208
Ser Ala Leu Gln Leu Leu Lys His Ser Phe Leu Glu Arg Ser His *
            725                 730                 735
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<210> 4
<211> 54
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<213> Artificial Sequence

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<223> PFAM protein kinase domain consensus sequence

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Gly Tyr Leu His His Arg Asp Leu Lys Asn Ile Leu Lys Asp Phe Gly
            20                  25                  30
Leu Ala Gly Thr Tyr Ala Pro Glu Asp Trp Ser Gly Leu Glu Pro Ser
        35                  40                  45
Leu Leu Asp Pro Arg Gly
    50
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<210> 5
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<212> PRT
<213> Artificial Sequence

<220>
<223> ATP binding region consensus sequence

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<223> Xaa = Any Amino Acid

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1               5                   10                  15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
            20                  25                  30
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